

=====

Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: Wed Jun 27 07:06:46 EDT 2007

=====

Application No: 10590457 Version No: 1.0

Input Set:**Output Set:**

Started: 2007-06-21 12:02:59.623
Finished: 2007-06-21 12:03:29.347
Elapsed: 0 hr(s) 0 min(s) 29 sec(s) 724 ms
Total Warnings: 116
Total Errors: 598
No. of SeqIDs Defined: 255
Actual SeqID Count: 255

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
E 300	Invalid codon found Leu SEQID (5) POS: 96
E 300	Invalid codon found Ser SEQID (5) POS: 100
E 300	Invalid codon found Ser SEQID (5) POS: 104
E 300	Invalid codon found Leu SEQID (5) POS: 108
E 300	Invalid codon found Lys SEQID (5) POS: 112
E 300	Invalid codon found Gly SEQID (5) POS: 116
E 300	Invalid codon found Glu SEQID (5) POS: 120
E 300	Invalid codon found Glu SEQID (5) POS: 124
E 300	Invalid codon found Val SEQID (5) POS: 128
E 300	Invalid codon found Cys SEQID (5) POS: 132
E 300	Invalid codon found Ile SEQID (5) POS: 136
E 300	Invalid codon found Asp SEQID (5) POS: 140
E 300	Invalid codon found Gly SEQID (5) POS: 144
E 300	Invalid codon found Ile SEQID (5) POS: 148
E 300	Invalid codon found Ile SEQID (5) POS: 152
E 300	Invalid codon found Tyr SEQID (5) POS: 156
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)

Input Set:

Output Set:

Started: 2007-06-21 12:02:59.623
Finished: 2007-06-21 12:03:29.347
Elapsed: 0 hr(s) 0 min(s) 29 sec(s) 724 ms
Total Warnings: 116
Total Errors: 598
No. of SeqIDs Defined: 255
Actual SeqID Count: 255

Input Set:

Output Set:

Started: 2007-06-21 12:02:59.623
Finished: 2007-06-21 12:03:29.347
Elapsed: 0 hr(s) 0 min(s) 29 sec(s) 724 ms
Total Warnings: 116
Total Errors: 598
No. of SeqIDs Defined: 255
Actual SeqID Count: 255

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (34)

Input Set:

Output Set:

Started: 2007-06-21 12:02:59.623
Finished: 2007-06-21 12:03:29.347
Elapsed: 0 hr(s) 0 min(s) 29 sec(s) 724 ms
Total Warnings: 116
Total Errors: 598
No. of SeqIDs Defined: 255
Actual SeqID Count: 255

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (40)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (42)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (44)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (45)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (45)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (50)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (64)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (82) POS (160)
W 213	Artificial or Unknown found in <213> in SEQ ID (115)
W 213	Artificial or Unknown found in <213> in SEQ ID (116)
W 213	Artificial or Unknown found in <213> in SEQ ID (121)
W 213	Artificial or Unknown found in <213> in SEQ ID (122)
W 213	Artificial or Unknown found in <213> in SEQ ID (123)

Input Set:

Output Set:

Started: 2007-06-21 12:02:59.623
Finished: 2007-06-21 12:03:29.347
Elapsed: 0 hr(s) 0 min(s) 29 sec(s) 724 ms
Total Warnings: 116
Total Errors: 598
No. of SeqIDs Defined: 255
Actual SeqID Count: 255

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (124)
W 213	Artificial or Unknown found in <213> in SEQ ID (125)
W 213	Artificial or Unknown found in <213> in SEQ ID (126)
W 213	Artificial or Unknown found in <213> in SEQ ID (127)
W 213	Artificial or Unknown found in <213> in SEQ ID (128)
W 213	Artificial or Unknown found in <213> in SEQ ID (129)
W 213	Artificial or Unknown found in <213> in SEQ ID (130)
W 213	Artificial or Unknown found in <213> in SEQ ID (139)
W 213	Artificial or Unknown found in <213> in SEQ ID (140)
W 213	Artificial or Unknown found in <213> in SEQ ID (141)
W 213	Artificial or Unknown found in <213> in SEQ ID (143)
W 213	Artificial or Unknown found in <213> in SEQ ID (144)
W 213	Artificial or Unknown found in <213> in SEQ ID (145)
W 213	Artificial or Unknown found in <213> in SEQ ID (146)
W 213	Artificial or Unknown found in <213> in SEQ ID (147) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (187)

SEQUENCE LISTING

<110> Cirpus, Petra
Bauer, Jorg
Qiu, Xiao
Wu, Guohai
Datla, Nagamani

<120> METHOD FOR PRODUCING POLYUNSATURATED FATTY ACIDS IN TRANSGENIC
PLANTS

<130> 13987-00020-US

<140> 10590457

<141> 2007-06-21

<150> 10/590,457

<151> 2006-08-25

<150> PCT/EP2005/001863

<151> 2005-02-23

<150> DE 10 2004 009 457.8

<151> 2004-02-27

<150> DE 10 2004 012 370.5

<151> 2004-03-13

<150> DE 10 2004 017 518.7

<151> 2004-04-08

<150> DE 10 2004 024 014.0

<151> 2004-05-14

<150> PCT/EP2004/07957

<151> 2004-07-16

<150> DE 10 2004 062 543.3

<151> 2004-12-24

<160> 255

<170> PatentIn version 3.4

<210> 1
<211> 1266
<212> DNA
<213> Euglena gracilis

<220>

<221> CDS

<222> (1)..(1266)

<223> Delta-8 desaturase

<400> 1

atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca

Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
1 5 10 15

tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att 96
Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
20 25 30

ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg 144
Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
35 40 45

cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat 192
His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
50 55 60

ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag 240
Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
65 70 75 80

gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat 288
Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
85 90 95

gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt 336
Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
100 105 110

gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att 384
Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
115 120 125

ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct 432
Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
130 135 140

cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac 480
His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
145 150 155 160

ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca 528
Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
165 170 175

tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa 576
Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
180 185 190

ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag 624
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
195 200 205

gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc 672
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe

210	215	220	
cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp 225 230 235 240			720
tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn 245 250 255			768
caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu 260 265 270			816
cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile 275 280 285			864
ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe 290 295 300			912
ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile 305 310 315 320			960
ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His 325 330 335			1008
gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly 340 345 350			1056
ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg 355 360 365			1104
cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys 370 375 380			1152
cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile 385 390 395 400			1200
ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro 405 410 415			1248
gcg ggg aag gct cta taa Ala Gly Lys Ala Leu 420			1266

<210> 2

<211> 421

<212> PRT

<213> Euglena gracilis

<400> 2

Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
1 5 10 15

Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
20 25 30

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
65 70 75 80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
85 90 95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
100 105 110

Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
115 120 125

Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
130 135 140

His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
145 150 155 160

Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
165 170 175

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
180 185 190

Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
195 200 205

Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
210 215 220

Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
225 230 235 240

Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
245 250 255

Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
260 265 270

His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
275 280 285

Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
290 295 300

Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
305 310 315 320

Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
325 330 335

Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
340 345 350

Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
355 360 365

His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
370 375 380

His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
385 390 395 400

Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro

405

410

415

Ala Gly Lys Ala Leu
420

<210> 3

<211> 777

<212> DNA

<213> Isochrysis galbana

<220>

<221> CDS

<222> (1)..(777)

<223> Delta-9 elongase

<400> 3

atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc 48
Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
1 5 10 15

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg 96
Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
20 25 30

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144
Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
35 40 45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192
Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
50 55 60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240
Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65 70 75 80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag 288
Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
85 90 95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag 336
Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
100 105 110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg	384
Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu	
115 120 125	
agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat	432
Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp	
130 135 140	
gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg	480
Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met	
145 150 155 160	
ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc	528
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Gly Leu	
165 170 175	
acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg	576
Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met	
180 185 190	
cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc	624
Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile	
195 200 205	
aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct	672
Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala	
210 215 220	
ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt	720
Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe	
225 230 235 240	
ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag	768
Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys	
245 250 255	
cag ctc tag	777
Gln Leu	

<210> 4

<211> 258

<212> PRT

<213> Isochrysis galbana

<400> 4

Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr	
1 5 10 15	

Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
20 25 30

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
35 40 45

Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
50 55 60

Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65 70 75 80

Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
85 90 95

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
100 105 110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
115 120 125

Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
130 135 140

Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
145 150 155 160

Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
165 170 175

Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
180 185 190

Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
195 200 205

Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
210 215 220

Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
225 230 235 240

Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
245 250 255

Gln Leu

<210> 5

<211> 1410

<212> DNA

<213> *Phaeodactylum tricornutum*

<220>

<221> CDS

<222> (1)..(1410)

<223> Delta-5 desaturase

<400> 5

atg gct ccg gat gcg gat aag ctt cga caa cgc cag acg act gcg gta 48
Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
1 5 10 15

gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt 96
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
20 25 30

ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat 144
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr

35 40 45

gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt 192
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
50 55 60

ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat 240
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
65 70 75 80